

**Influence of temperature on BTV-8 transmission in NW-Europe in 2007**

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A temperature limit for bluetongue virus (BTV) transmission has been established from the data of the 2006 BTV-8 epidemic. That analysis showed that the temperature threshold required for transmission between livestock herds was about 15 °C. This result was considered to be specific for the situation in NW-Europe in 2006, and it remained unknown, whether and how these results can be extrapolated to different conditions. We analysed the 2007 BTV-8 epidemic data with the same method, and compared the results from the two years, to derive more insight into the impact of some of the more uncertain variables. We established that the method needed to be extended with a correction, for the fact that the advancing epidemic could no longer be evaluated as a starting epidemic. Especially in Belgium, many farms were already infected in 2006, which causes reduced transmission levels, due to dilution of susceptible farms. After correcting for the fraction of remaining susceptible farms, we found that the threshold temperature at which the infection spreads between herds again lies at 15 °C. So we have validated the previous results as being far more general than expected, and not only relevant for the specific situation in 2006. The consistency of both results, despite being derived from a different year, a different temperature profile during the year and a larger area of concern, proves that this conclusion is quite robust. In conclusion, these results can be used for extrapolation to other years and regions, while considering that a similar type of animal husbandry, similar host density and similar *Culicoides* species involved are probably still a requirement for a valid extrapolation.

**Identifying sources of heteroskedasticity of average daily weight gain in commercial feedlot cattle using a hierarchical Bayesian approach**

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The objectives of the present study were to assess the heterogeneity of variance in average daily weight gain (ADG) in commercial feedlot cattle cohorts, and to identify demographic factors as potential sources of cohort- and feedlot-level heteroskedasticity in ADG. An operational dataset compiled from 25 U.S. commercial feedlots containing 24,050 cohorts from 2005 and 2006 was utilized for this study. Inference was based on a hierarchical Bayesian model implemented with Markov Chain Monte Carlo, whereby cohorts were modeled at the residual level and feedlot-years were modeled as clustering random effects. Forward model selection based on Deviance Information Criterion was used to screen potentially important explanatory variables for cohort- and feedlot-level heteroskedasticity. The Bayesian modeling framework was preferred as it naturally accommodates the inherently hierarchical structure of feedlot data whereby cohorts are nested within feedlot-year clusters. Heterogeneity of variance was primarily concentrated at the cohort-level. Feedlot-year specific effects were, by far, the greatest contributors to ADG heteroskedasticity amongst cohorts. In addition, identifiable demographic factors associated with between-cohort variances included cohort size, arrival season, days on feed and mean arrival weight. These results indicate the need for further investigation of sources of heteroskedasticity in feedlot performance in order to increase consistency of beef production outcomes as well as enhance efficiency of statistical inference on treatment effects.